SEQUENCE LISTING

```
<110> PLOWMAN, GREGORY D.
      WHYTE, DAVID
      MANNING, GERARD
<120> NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
      GENOMIC SEQUENCING
<130> 038602/1277
<140> 09/986,992
<141> 2001-11-13
<150> 60/246,974
<151> 2000-11-13
<150> 60/208,291
<151> 2000-05-30
<160> 2
<170> PatentIn Ver. 2.1
<210> 1
<211> 1119
<212> DNA
<213> Homo sapiens
<400> 1
atgtcaacag ctgccttaat tactttggtc agaagtggtg ggaaccaggt gagaaggaga 60
gtgctgctaa gctcccgcct gctgcaggac gacaggcggg tgacacccac gtgccacagc 120
tccacttcag agcctaggtg ttctcggttt gacccagatg gtagtgggag tccagctacc 180
tgggacaatt ttgggatctg ggataaccgc attgatgagc caattctgct gccacccagc 240
attaagtatg gcaagccaat tcccaaaatc agcttggaaa atgtggggtg cgcctcacag 300
attggcaaac ggaaagagaa tgaagatcgg tttgacttcg ctcagctgac agatgaggtc 360
ctgtactttg cagtgtatga tggacacggt ggacctgcag cagctgattt ctgtcatacc 420
cacatggaga aatgtattat ggatttgctt cctaaggaga agaacttgga aactctgttg 480
accttggctt ttctagaaat agataaagcc ttttcgagtc atgcccgcct gtctgctgat 540
gcaactette tgacetetgg gactaetgca acagtagece tattgcgaga tggtattgaa 600
ctggttgtag ccagtgttgg ggacagccgg gctattttgt gtagaaaagg aaaacccatg 660
aagctgacca ttgaccatac tccagaaaga aaagatgaaa aagaaaggat caagaaatgt 720
ggtggttttg tagcttggaa tagtttgggg cagcctcacg taaatggcag gcttgcaatg 780
acaagaagta ttggagattt ggaccttaag accagtggtg tcatagcaga acctgaaact 840
aagaggatta agttacatca tgctgatgac agcttcctgg tcctcaccac agatggaatt 900
aacttcatgg tgaatagtca agagatttgt qactttqtca atcaqtqcca tqatcccaac 960
gaagcagccc atgcggtgac tgaacaggca atacagtacg gtactgagga taacagtact 1020
gcagtagtag tgccttttgg tgcctgggga aaatataaga actctgaaat caacttctca 1080
ttcagcagaa gctttgcctc cagtggacga tgggcctga
<210> 2
<211> 372
<212> PRT
```

<213> Homo sapiens

<400> 2 Met Ser Thr Ala Ala Leu Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys His Ser Ser Thr Ser Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly 120 His Gly Gly Pro Ala Ala Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu 155 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg 165 170 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val 185 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys 230 235 Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser 265 Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala

Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val

295

Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn 305 310 315 320

Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu 325 330 335

Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr 340 345 350

Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser 355 360 365

Gly Arg Trp Ala 370